

SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger
 <120> Novel chimeric plasminogen activators and their pharmaceutical use
 <160> 13

<210> 1
 <211> 1143
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1143)
 <223> Coding sequence of the surfactant protein B precursor

<400> 1

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| atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg | 48 |
| Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr | |
| 1 5 10 15 | |
| ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt | 96 |
| Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys | |
| 20 25 30 | |
| gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag | 144 |
| Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln | |
| 35 40 45 | |
| tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga | 192 |
| Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly | |
| 50 55 60 | |
| gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac | 240 |
| Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn | |
| 65 70 75 80 | |
| aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg | 288 |
| Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu | |
| 85 90 95 | |
| gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc | 336 |
| Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys | |
| 100 105 110 | |
| aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag | 384 |
| Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln | |
| 115 120 125 | |
| aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa | 432 |
| Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys | |
| 130 135 140 | |
| tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg | 480 |
| Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu | |
| 145 150 155 160 | |
| ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc | 528 |

| | |
|---|------|
| Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu | |
| 165 170 175 | |
| gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac | 576 |
| Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His | |
| 180 185 190 | |
| aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc | 624 |
| Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys | |
| 195 200 205 | |
| tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag | 672 |
| Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys | |
| 210 215 220 | |
| ggg ggc cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg | 720 |
| Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu | |
| 225 230 235 240 | |
| gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc | 768 |
| Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile | |
| 245 250 255 | |
| ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc | 816 |
| Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg | |
| 260 265 270 | |
| ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg | 864 |
| Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro | |
| 275 280 285 | |
| aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc | 912 |
| Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser | |
| 290 295 300 | |
| gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca | 960 |
| Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala | |
| 305 310 315 320 | |
| atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag | 1008 |
| Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys | |
| 325 330 335 | |
| caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg | 1056 |
| Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg | |
| 340 345 350 | |
| ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc | 1104 |
| Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr | |
| 355 360 365 | |
| atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt | 1143 |
| Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu | |
| 370 375 380 | |

<210> 2

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<400> 2

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atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg      48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
  1              5              10              15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt      96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
      20              25              30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag      144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
      35              40              45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga      192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
      50              55              60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac      240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
      65              70              75              80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg      288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
      85              90              95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc      336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
      100             105             110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag      384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
      115             120             125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa      432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
      130             135             140

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg      480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
      145             150             155             160

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc      528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
      165             170             175

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac      576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
      180             185             190

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc      624

```

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Thr | Gln | Asp | Leu | Ser | Glu | Gln | Gln | Phe | Pro | Ile | Pro | Leu | Pro | Tyr | Cys | | |
| | 195 | | | | | | 200 | | | | | 205 | | | | | |
| tgg | ctc | tgc | agg | gct | ctg | atc | aag | cgg | atc | caa | gcc | atg | att | ccc | aag | | 672 |
| Trp | Leu | Cys | Arg | Ala | Leu | Ile | Lys | Arg | Ile | Gln | Ala | Met | Ile | Pro | Lys | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| ggt | gcg | cta | gct | gtg | gca | gtg | gcc | cag | gtg | tgc | cgc | gtg | gta | cct | ctg | | 720 |
| Gly | Ala | Leu | Ala | Val | Ala | Val | Ala | Gln | Val | Cys | Arg | Val | Val | Pro | Leu | | |
| | 225 | | | | 230 | | | | | 235 | | | | 240 | | | |
| gtg | gcg | ggc | ggc | atc | tgc | cag | tgc | ctg | gct | gag | cgc | tac | tcc | gtc | atc | | 768 |
| Val | Ala | Gly | Gly | Ile | Cys | Gln | Cys | Leu | Ala | Glu | Arg | Tyr | Ser | Val | Ile | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| ctg | ctc | gac | acg | ctg | ctg | ggc | cgc | atg | ctg | ccc | cag | ctg | gtc | tgc | cgc | | 816 |
| Leu | Leu | Asp | Thr | Leu | Leu | Gly | Arg | Met | Leu | Pro | Gln | Leu | Val | Cys | Arg | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| ctc | gtc | ctc | cgg | tgc | tcc | atg | | | | | | | | | | | 837 |
| Leu | Val | Leu | Arg | Cys | Ser | Met | | | | | | | | | | | |
| | | | 275 | | | | | | | | | | | | | | |

<210> 3
 <211> 237
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1) ... (237)
 <223> Coding sequence of the mature surfactant protein B

 <400> 3

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| ttc | ccc | att | cct | ctc | ccc | tat | tgc | tgg | ctc | tgc | agg | gct | ctg | atc | aag | | 48 |
| Phe | Pro | Ile | Pro | Leu | Pro | Tyr | Cys | Trp | Leu | Cys | Arg | Ala | Leu | Ile | Lys | | |
| | 1 | | | 5 | | | | 10 | | | | | 15 | | | | |
| cgg | atc | caa | gcc | atg | att | ccc | aag | ggt | gcg | cta | gct | gtg | gca | gtg | gcc | | 96 |
| Arg | Ile | Gln | Ala | Met | Ile | Pro | Lys | Gly | Ala | Leu | Ala | Val | Ala | Val | Ala | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| cag | gtg | tgc | cgc | gtg | gta | cct | ctg | gtg | gcg | ggc | ggc | atc | tgc | cag | tgc | | 144 |
| Gln | Val | Cys | Arg | Val | Val | Pro | Leu | Val | Ala | Gly | Gly | Ile | Cys | Gln | Cys | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | |
| ctg | gct | gag | cgc | tac | tcc | gtc | atc | ctg | ctc | gac | acg | ctg | ctg | ggc | cgc | | 192 |
| Leu | Ala | Glu | Arg | Tyr | Ser | Val | Ile | Leu | Leu | Asp | Thr | Leu | Leu | Gly | Arg | | |
| | | 50 | | | | 55 | | | | 60 | | | | | | | |
| atg | ctg | ccc | cag | ctg | gtc | tgc | cgc | ctc | gtc | ctc | cgg | tgc | tcc | atg | | | 237 |
| Met | Leu | Pro | Gln | Leu | Val | Cys | Arg | Leu | Val | Leu | Arg | Cys | Ser | Met | | | |
| | 65 | | | | 70 | | | | | 75 | | | | | | | |

<210> 4
 <211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

<400> 4

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|---|-----|
| atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc | 48 |
| Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser | |
| 1 5 10 15 | |
| gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac | 96 |
| Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp | |
| 20 25 30 | |
| tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att | 144 |
| Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile | |
| 35 40 45 | |
| cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata | 192 |
| His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile | |
| 50 55 60 | |
| gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga | 240 |
| Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly | |
| 65 70 75 80 | |
| aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct | 288 |
| Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser | |
| 85 90 95 | |
| gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt | 336 |
| Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu | |
| 100 105 110 | |
| cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg | 384 |
| Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg | |
| 115 120 125 | |
| agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa | 432 |
| Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln | |
| 130 135 140 | |
| gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct | 480 |
| Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro | |
| 145 150 155 160 | |
| cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc | 528 |
| Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg | |
| 165 170 175 | |
| ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg | 576 |
| Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp | |
| 180 185 190 | |
| ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg | 624 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| Phe | Ala | Ala | Ile | Tyr | Arg | Arg | His | Arg | Gly | Gly | Ser | Val | Thr | Tyr | Val | | |
| | 195 | | | | | | 200 | | | | | 205 | | | | | |
| tgt | gga | ggc | agc | ctc | atc | agc | cct | tgc | tgg | gtg | atc | agc | gcc | aca | cac | | 672 |
| Cys | Gly | Gly | Ser | Leu | Ile | Ser | Pro | Cys | Trp | Val | Ile | Ser | Ala | Thr | His | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| tgc | ttc | att | gat | tac | cca | aag | aag | gag | gac | tac | atc | gtc | tac | ctg | ggt | | 720 |
| Cys | Phe | Ile | Asp | Tyr | Pro | Lys | Lys | Glu | Asp | Tyr | Ile | Val | Tyr | Leu | Gly | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| cgc | tca | agg | ctt | aac | tcc | aac | acg | caa | ggg | gag | atg | aag | ttt | gag | gtg | | 768 |
| Arg | Ser | Arg | Leu | Asn | Ser | Asn | Thr | Gln | Gly | Glu | Met | Lys | Phe | Glu | Val | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| gaa | aac | ctc | atc | cta | cac | aag | gac | tac | agc | gct | gac | acg | ctt | gct | cac | | 816 |
| Glu | Asn | Leu | Ile | Leu | His | Lys | Asp | Tyr | Ser | Ala | Asp | Thr | Leu | Ala | His | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | |
| cac | aac | gac | att | gcc | ttg | ctg | aag | atc | cgt | tcc | aag | gag | ggc | agg | tgt | | 864 |
| His | Asn | Asp | Ile | Ala | Leu | Leu | Lys | Ile | Arg | Ser | Lys | Glu | Gly | Arg | Cys | | |
| | | 275 | | | | | 280 | | | | | | 285 | | | | |
| gcg | cag | cca | tcc | cgg | act | ata | cag | acc | atc | tgc | ctg | ccc | tcg | atg | tat | | 912 |
| Ala | Gln | Pro | Ser | Arg | Thr | Ile | Gln | Thr | Ile | Cys | Leu | Pro | Ser | Met | Tyr | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| aac | gat | ccc | cag | ttt | ggc | aca | agc | tgt | gag | atc | act | ggc | ttt | gga | aaa | | 960 |
| Asn | Asp | Pro | Gln | Phe | Gly | Thr | Ser | Cys | Glu | Ile | Thr | Gly | Phe | Gly | Lys | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| gag | aat | tct | acc | gac | tat | ctc | tat | ccg | gag | cag | ctg | aaa | atg | act | gtt | | 1008 |
| Glu | Asn | Ser | Thr | Asp | Tyr | Leu | Tyr | Pro | Glu | Gln | Leu | Lys | Met | Thr | Val | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| gtg | aag | ctg | att | tcc | cac | cgg | gag | tgt | cag | cag | ccc | cac | tac | tac | ggc | | 1056 |
| Val | Lys | Leu | Ile | Ser | His | Arg | Glu | Cys | Gln | Gln | Pro | His | Tyr | Tyr | Gly | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| tct | gaa | gtc | acc | acc | aaa | atg | ctg | tgt | gct | gct | gac | cca | cag | tgg | aaa | | 1104 |
| Ser | Glu | Val | Thr | Thr | Lys | Met | Leu | Cys | Ala | Ala | Asp | Pro | Gln | Trp | Lys | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| aca | gat | tcc | tgc | cag | gga | gac | tca | ggg | gga | ccc | ctc | gtc | tgt | tcc | ctc | | 1152 |
| Thr | Asp | Ser | Cys | Gln | Gly | Asp | Ser | Gly | Gly | Pro | Leu | Val | Cys | Ser | Leu | | |
| | | 370 | | | | 375 | | | | | 380 | | | | | | |
| caa | ggc | cgc | atg | act | ttg | act | gga | att | gtg | agc | tgg | ggc | cgt | gga | tgt | | 1200 |
| Gln | Gly | Arg | Met | Thr | Leu | Thr | Gly | Ile | Val | Ser | Trp | Gly | Arg | Gly | Cys | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | |
| gcc | ctg | aag | gac | aag | cca | ggc | gtc | tac | acg | aga | gtc | tca | cac | ttc | tta | | 1248 |
| Ala | Leu | Lys | Asp | Lys | Pro | Gly | Val | Tyr | Thr | Arg | Val | Ser | His | Phe | Leu | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| ccc | tgg | atc | cgc | agt | cac | acc | aag | gaa | gag | aat | ggc | ctg | gcc | ctc | | | 1293 |
| Pro | Trp | Ile | Arg | Ser | His | Thr | Lys | Glu | Gln | Asn | Gly | Leu | Ala | Leu | | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |

<210> 5
 <211> 828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (828)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 5

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| aag ccc tcc tct cct cca gaa gaa tta aaa ttt cag tgt ggc caa aag | 48 |
| Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys | |
| 1 5 10 15 | |
| act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc | 96 |
| Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile | |
| 20 25 30 | |
| gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc | 144 |
| Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly | |
| 35 40 45 | |
| tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg | 192 |
| Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val | |
| 50 55 60 | |
| atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac | 240 |
| Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr | |
| 65 70 75 80 | |
| atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag | 288 |
| Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu | |
| 85 90 95 | |
| atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct | 336 |
| Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala | |
| 100 105 110 | |
| gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc | 384 |
| Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser | |
| 115 120 125 | |
| aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc | 432 |
| Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys | |
| 130 135 140 | |
| ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc | 480 |
| Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile | |
| 145 150 155 160 | |
| act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag | 528 |
| Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln | |
| 165 170 175 | |
| ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag | 576 |

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Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln
      180                      185                      190

ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct      624
Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala
      195                      200                      205

gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc      672
Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
      210                      215                      220

ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc      720
Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser
      225                      230                      235                      240

tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga      768
Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg
      245                      250                      255

gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat      816
Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn
      260                      265                      270

ggc ctg gcc ctc
Gly Leu Ala Leu
      275

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<210> 6

<211> 1671

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>

<221> CDS

<222> (844) ... (1671)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 6

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atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg      48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr
      1                      5                      10                      15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt      96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
      20                      25                      30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag      144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
      35                      40                      45

```


| | |
|---|-----|
| tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly 50 55 60 | 192 |
| gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn 65 70 75 80 | 240 |
| aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu 85 90 95 | 288 |
| gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys 100 105 110 | 336 |
| aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln 115 120 125 | 384 |
| aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys 130 135 140 | 432 |
| tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu 145 150 155 160 | 480 |
| ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu 165 170 175 | 528 |
| gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His 180 185 190 | 576 |
| aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys 195 200 205 | 624 |
| tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys 210 215 220 | 672 |
| ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu 225 230 235 240 | 720 |
| gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile 245 250 255 | 768 |
| ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg 260 265 270 | 816 |
| ctc gtc ctc cgg tgc tcc atg aag ctt aag ccc tcc tct cct cca gaa Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu 275 280 285 | 864 |

| | |
|---|------|
| gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys 290 295 300 | 912 |
| att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala 305 310 315 320 | 960 |
| gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly 325 330 335 | 1008 |
| ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe 340 345 350 | 1056 |
| att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser 355 360 365 | 1104 |
| agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn 370 375 380 | 1152 |
| ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn 385 390 395 400 | 1200 |
| gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln 405 410 415 | 1248 |
| cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp 420 425 430 | 1296 |
| ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn 435 440 445 | 1344 |
| tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys 450 455 460 | 1392 |
| ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu 465 470 475 480 | 1440 |
| gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp 485 490 495 | 1488 |
| tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly 500 505 510 | 1536 |
| cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu | 1584 |

515 520 525

aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg 1632
 Lys Asp Lys Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp
 530 535 540

atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc 1671
 Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu
 545 550 555

<210> 7
 <211> 1674
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) ... (837)
) <223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> CDS
 <222> (847) ... (1674)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 7

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg 48
 Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
 1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
 20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
 35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
 50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
 85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc 336
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
 100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384

| | |
|---|------|
| Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln | |
| 115 120 125 | |
| aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa | 432 |
| Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys | |
| 130 135 140 | |
| tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg | 480 |
| Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu | |
| 145 150 155 160 | |
| ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc | 528 |
| Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu | |
| 165 170 175 | |
| gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac | 576 |
| Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His | |
| 180 185 190 | |
| aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc | 624 |
| Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys | |
| 195 200 205 | |
| tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag | 672 |
| Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys | |
| 210 215 220 | |
| ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg | 720 |
| Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu | |
| 225 230 235 240 | |
| gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc | 768 |
| Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile | |
| 245 250 255 | |
| ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc | 816 |
| Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg | |
| 260 265 270 | |
| ctc gtc ctc cgg tgc tcc atg cag ata tct aag ccc tcc tct cct cca | 864 |
| Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro | |
| 275 280 285 | |
| gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt | 912 |
| Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe | |
| 290 295 300 | |
| aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt | 960 |
| Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe | |
| 305 310 315 320 | |
| gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt | 1008 |
| Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys | |
| 325 330 335 | |
| gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc | 1056 |
| Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys | |
| 340 345 350 | |

ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc 1104
 Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg
 355 360 365

tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa 1152
 Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu
 370 375 380

aac ctg atc cta cac aag gac tac agc gct gac acg ctt gct cac cac 1200
 Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His
 385 390 395 400

aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg 1248
 Asn Asp Ile Ala Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala
 405 410 415

cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac 1296
 Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn
 420 425 430

gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag 1344
 Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu
 435 440 445

aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg 1392
 Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val
 450 455 460

aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct 1440
 Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser
 465 470 475 480

gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca 1488
 Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr
 485 490 495

gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa 1536
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln
 500 505 510

ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc 1584
 Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala
 515 520 525

ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc 1632
 Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro
 530 535 540

tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc 1674
 Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu
 545 550 555

<210> 8

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (591)

<223> Coding sequence of the surfactant protein C precursor

<400> 8

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atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac      48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
  1             5             10             15

tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac      96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
          20             25             30

ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtc ctc atc gtc gtg      144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val
          35             40             45

gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac      192
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His
          50             55             60

acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa      240
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln
          65             70             75             80

cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc      288
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile
          85             90             95

ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc      336
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala
          100            105            110

tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca      384
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro
          115            120            125

gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc      432
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe
          130            135            140

cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag      480
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys
          145            150            155            160

ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg      528
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly
          165            170            175

gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg      576
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val
          180            185            190

ccg ctc tac tac atc      591
Pro Leu Tyr Tyr Ile
          195

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<210> 9
 <211> 174
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1) ... (174)
 <223> Coding sequence of the surfactant protein C precursor lacking the C-terminal propeptide

<400> 9

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|---|-----|
| atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac | 48 |
| Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr | |
| 1 5 10 15 | |
| tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac | 96 |
| Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His | |
| 20 25 30 | |
| ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg | 144 |
| Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val | |
| 35 40 45 | |
| gtg att gtg gga gcc ctg ctc atg ggt ctc | 174 |
| Val Ile Val Gly Ala Leu Leu Met Gly Leu | |
| 50 55 | |

<210> 10
 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (105)
 <223> Coding sequence of the mature surfactant protein C

<400> 10

| | |
|---|-----|
| ttt ggc att ccc tgc tgc cca gtg cac ctg aaa cgc ctt ctt atc gtg | 48 |
| Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val | |
| 1 5 10 15 | |
| gtg gtg gtg gtg gtc ctc atc gtc gtg gtg att gtg gga gcc ctg ctc | 96 |
| Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu | |
| 20 25 30 | |
| atg ggt ctc | 105 |
| Met Gly Leu | |
| 35 | |

<210> 11
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1686)

<223> Coding sequence of the tissue-plasminogen activator

<400> 11

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atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga      48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
  1              5              10              15

gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga      96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
          20              25              30

gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg      144
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
          35              40              45

ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac      192
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
          50              55              60

cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca      240
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
          65              70              75              80

gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc      288
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
          85              90              95

tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa      336
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
          100              105              110

gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac      384
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
          115              120              125

gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt      432
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
          130              135              140

ggc gcc gag tgc acc aac tgg aac agc agc gcg ttg gcc cag aag ccc      480
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
          145              150              160              165

tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac      528
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
          170              175              180

aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc      576
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
          185              190              195

ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc      624
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
          200              205              205

```


| | |
|---|------|
| tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg 210 215 220 | 672 |
| ggc acg cac agc ctc acc gag tgc ggt gcc tcc tgc ctc ccg tgg aat Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn 225 230 235 240 | 720 |
| tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala 245 250 255 | 768 |
| cag gca ctg ggc ctg ggc aaa cat aat tac tgc cgg aat cct gat ggg Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly 260 265 270 | 816 |
| gat gcc aag ccc tgg tgc cac gtg ctg aag aac cgc agg ctg acg tgg Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp 275 280 285 | 864 |
| gag tac tgt gat gtg ccc tcc tgc tcc acc tgc ggc ctg aga cag tac Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr 290 295 300 | 912 |
| agc cag cct cag ttt cgc atc aaa gga ggg ctc ttc gcc gac atc gcc Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala 305 310 315 320 | 960 |
| tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro 325 330 335 | 1008 |
| gga gag cgg ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile 340 345 350 | 1056 |
| ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu 355 360 365 | 1104 |
| acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu 370 375 380 | 1152 |
| cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp 385 390 395 400 | 1200 |
| gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser 405 410 415 | 1248 |
| tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro 420 425 430 | 1296 |
| ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly 435 440 445 | 1344 |

| 435 | 440 | 445 | |
|---|-----|-----|------|
| tac ggc aag cat gag gcc ttg tct cct ttc tat tcg gag cgg ctg aag | | | 1392 |
| Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys | | | |
| 450 | 455 | 460 | |
| gag gct cat gtc aga ctg tac cca tcc agc cgc tgc aca tca caa cat | | | 1440 |
| Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His | | | |
| 465 | 470 | 475 | 480 |
| tta ctt aac aga aca gtc acc gac aac atg ctg tgt gct gga gac act | | | 1488 |
| Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr | | | |
| | 485 | 490 | 495 |
| cgg agc ggc ggg ccc cag gca aac ttg cac gac gcc tgc cag ggc gat | | | 1536 |
| Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp | | | |
| | 500 | 505 | 510 |
| tcg gga ggc ccc ctg gtg tgt ctg aac gat ggc cgc atg act ttg gtg | | | 1584 |
| Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val | | | |
| | 515 | 520 | 525 |
| ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt | | | 1632 |
| Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly | | | |
| | 530 | 535 | 540 |
| gtg tac acc aag gtt acc aac tac cta gac tgg att cgt gac aac atg | | | 1680 |
| Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met | | | |
| 545 | 550 | 555 | 560 |
| cga ccg | | | 1686 |
| Arg Pro | | | |

<210> 12
 <211> 1158
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> sig_peptide
 <222> (1) ... (69)
 <223> Signal sequence of the surfactant protein B

<220>
 <221> CDS
 <222> (76) ... (312)
 <223> Coding sequence of the mature surfactant protein B

<220>
 <221> CDS
 <222> (313) ... (1140)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> CDS
 <222> (1141) ... (1158)
 <223> Hexahistidin affinity tag

<400> 12

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|---|-----|
| atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg | 48 |
| Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr | |
| 1 5 10 15 | |
| ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat | 96 |
| Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr | |
| 20 25 30 | |
| tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc | 144 |
| Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro | |
| 35 40 45 | |
| aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct | 192 |
| Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro | |
| 50 55 60 | |
|) ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc | 240 |
| Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val | |
| 65 70 75 80 | |
| atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc | 288 |
| Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys | |
| 85 90 95 | |
| cgc ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa gaa | 336 |
| Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu | |
| 100 105 110 | |
| tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att | 384 |
| Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile | |
| 115 120 125 | |
| att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc | 432 |
| Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala | |
| 130 135 140 | |
|) atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc | 480 |
| Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly | |
| 145 150 155 160 | |
| agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att | 528 |
| Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile | |
| 165 170 175 | |
| gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg | 576 |
| Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg | |
| 180 185 190 | |
| ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc | 624 |
| Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu | |
| 195 200 205 | |
| atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac | 672 |
| Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp | |
| 210 215 220 | |

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att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca      720
Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro
225                230                235                240

tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc      768
Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro
                245                250                255

cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct      816
Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser
                260                265                270

acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg      864
Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu
                275                280                285

att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc      912
Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val
                290                295                300

acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc      960
Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
305                310                315                320

tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc      1008
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
                325                330                335

atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag      1056
Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
                340                345                350

gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc      1104
Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
                355                360                365

cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat      1152
Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His
                370                375                380

cat cat
His His
385

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<210> 13

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<221> sig_peptide

<222> (1) ... (60)

<223> Signal sequence of the urokinase plasminogen activator

<220>

<221> CDS

<222> (67) ... (894)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> CDS

<222> (895) ... (1131)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> CDS

<222> (1132) ... (1149)

<223> Hexahistidin affinity tag

<400> 13

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| atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc | 48 |
| Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser | |
| 1 5 10 15 | |
| gac tcc aaa ggc agc aat aag ccc tcc tct cct cca gaa gaa tta aaa | 96 |
| Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys | |
| 20 25 30 | |
| ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att att ggg | 144 |
| Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly | |
| 35 40 45 | |
| gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc atc tac | 192 |
| Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr | |
| 50 55 60 | |
| agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc agc ctc | 240 |
| Arg Arg His Arg Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu | |
| 65 70 75 80 | |
| atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att gat tac | 288 |
| Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr | |
| 85 90 95 | |
| cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg ctt aac | 336 |
| Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn | |
| 100 105 110 | |
| tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc atc cta | 384 |
| Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu | |
| 115 120 125 | |
| cac aag gac tac agc gct gac acg ctt gct cac cac aac gac att gcc | 432 |
| His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala | |
| 130 135 140 | |
| ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca tcc cgg | 480 |
| Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg | |
| 145 150 155 160 | |
| act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc cag ttt | 528 |
| Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe | |
| 165 170 175 | |

| | |
|---|------|
| ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct acc gac | 576 |
| Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp | |
| 180 185 190 | |
| tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc | 624 |
| Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser | |
| 195 200 205 | |
| cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc acc acc | 672 |
| His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr | |
| 210 215 220 | |
| aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc tgc cag | 720 |
| Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln | |
| 225 230 235 240 | |
| gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc atg act | 768 |
| Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr | |
| 245 250 255 | |
| ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag gac aag | 816 |
| Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys | |
| 260 265 270 | |
| cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt | 864 |
| Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser | |
| 275 280 285 | |
| cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc | 912 |
| His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro | |
| 290 295 300 | |
| tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att | 960 |
| Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile | |
| 305 310 315 320 | |
| ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta | 1008 |
| Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val | |
| 325 330 335 | |
| cct ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc | 1056 |
| Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser | |
| 340 345 350 | |
| gtc atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc | 1104 |
| Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val | |
| 355 360 365 | |
| tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat | 1149 |
| Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His | |
| 370 375 380 | |